

SEQUENCE LISTING

<110> Biogen, Inc.
 Burkly, Linda
 Wang, Li Chun

<120> METHODS OF MODULATING LIPID METABOLISM AND STORAGE

<130> A069PCT

<140> PCT/US00/05662

<141> 2000-03-03

<150> 60/122,640

<151> 1999-03-03

<150> 60/124,446

<151> 1999-03-15

<160> 22

<170> PatentIn Ver. 2.1

<210> 1

<211> 1277

<212> DNA

<213> Gallus sp.

<220>

<221> CDS

<222> (1)..(1275)

<400> 1

atg gtc gaa atg ctg ctg ttg aca aga att ctc ttg gtg ggc ttc atc 48

Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile
 1 5 10 15

tgc gct ctt tta gtc tcc tct ggg ctg act tgt gga cca ggc agg ggc 96

Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly
 20 25 30

att gga aaa agg agg cac ccc aaa aag ctg acc ccg tta gcc tat aag 144

Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
 35 40 45

cag ttt att ccc aat gtg gca gag aag acc cta ggg gcc agt gga aga 192

Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg

a069seq

50		55		60	
tat gaa ggg aag atc aca aga aac tcc gag aga ttt aaa gaa cta acc					240
Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr	65	70	75	80	
cca aat tac aac cct gac att att ttt aag gat gaa gag aac acg gga					288
Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly		85	90	95	
gct gac aga ctg atg act cag cgc tgc aag gac aag ctg aat gcc ctg					336
Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu		100	105	110	
gcg atc tcg gtg atg aac cag tgg ccc ggg gtg aag ctg cgg gtg acc					384
Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr		115	120	125	
gag ggc tgg gac gag gat ggc cat cac tcc gag gaa tcg ctg cac tac					432
Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr	130	135	140		
gag ggt cgc gcc gtg gac atc acc acg tcg gat cgg gac cgc agc aag					480
Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys	145	150	155	160	
tac gga atg ctg gcc cgc ctc gcc gtc gag gcc ggc ttc gac tgg gtc					528
Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val		165	170	175	
tac tac gag tcc aag gcg cac atc cac tgc tcc gtc aaa gca gaa aac					576
Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn		180	185	190	
tca gtg gca gcg aaa tca gga ggc tgc ttc cct ggc tca gcc aca gtg					624
Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val		195	200	205	
cac ctg gag cat gga ggc acc aag ctg gtg aag gac ctg agc cct ggg					672
His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly	210	215	220		

a069seq

gac cgc gtg ctg gct gct gac gcg gac ggc cgg ctg ctc tac agt gac	720
Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp	
225 230 235 240	
ttc ctc acc ttc ctc gac cgg atg gac agc tcc cga aag ctc ttc tac	768
Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr	
245 250 255	
gtc atc gag acg cgg cag ccc cgg gcc cgg ctg cta ctg acg gcg gcc	816
Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala	
260 265 270	
cac ctg ctc ttt gtg gcc ccc cag cac aac cag tcg gag gcc aca ggg	864
His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly	
275 280 285	
tcc acc agt ggc cag gcg ctc ttc gcc agc aac gtg aag cct ggc caa	912
Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln	
290 295 300	
cgt gtc tat gtg ctg ggc gag ggc ggg cag cag ctg ctg ccg gcg tct	960
Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser	
305 310 315 320	
gtc cac agc gtc tca ttg cgg gag gag gcg tcc gga gcc tac gcc cca	1008
Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro	
325 330 335	
ctc acc gcc cag ggc acc atc ctc atc aac cgg gtg ttg gcc tcc tgc	1056
Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys	
340 345 350	
tac gcc gtc atc gag gag cac agt tgg gcc cat tgg gcc ttc gca cca	1104
Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro	
355 360 365	
ttc cgc ttg gct cag ggg ctg ctg gcc gcc ctc tgc cca gat ggg gcc	1152
Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala	
370 375 380	

```

                                a069seq
atc cct act gcc gcc acc acc acc act ggc atc cat tgg tac tca cgg      1200
Ile Pro Thr Ala Ala Thr Thr Thr Thr Gly Ile His Trp Tyr Ser Arg
385                               390                               395                               400

ctc ctc tac cgc atc ggc agc tgg gtg ctg gat ggt gac gcg ctg cat      1248
Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
                               405                               410                               415

ccg ctg ggc atg gtg gca ccg gcc agc tg                                1277
Pro Leu Gly Met Val Ala Pro Ala Ser
                               420                               425

<210> 2
<211> 1190
<212> DNA
<213> Murine sp.

<220>
<221> CDS
<222> (1)..(1188)

<400> 2
atg gct ctg ccg gcc agt ctg ttg ccc ctg tgc tgc ttg gca ctc ttg      48
Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
  1                               5                               10                               15

gca cta tct gcc cag agc tgc ggg ccg ggc cga gga ccg gtt ggc cgg      96
Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
                               20                               25                               30

cgg cgt tat gtg cgc aag caa ctt gtg cct ctg cta tac aag cag ttt      144
Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
                               35                               40                               45

gtg ccc agt atg ccc gag cgg acc ctg ggc gcg agt ggg cca gcg gag      192
Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
                               50                               55                               60

ggg agg gta aca agg ggg tcg gag cgc ttc cgg gac ctc gta ccc aac      240
Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
  65                               70                               75                               80

tac aac ccc gac ata atc ttc aag gat gag gag aac agc ggc gca gac      288

```

a069seq

Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Ser	Gly	Ala	Asp	
				85					90					95		
cg	ct	at	gc	gag	cgt	tgc	aaa	gag	cgg	gtg	aac	gct	cta	gcc	atc	336
Arg	Leu	Met	Thr	Glu	Arg	Cys	Lys	Glu	Arg	Val	Asn	Ala	Leu	Ala	Ile	
			100					105					110			
gc	gt	at	gc	atg	tgg	ccc	gga	gta	cgc	cta	cgt	gtg	act	gaa	ggc	384
Ala	Val	Met	Asn	Met	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly	
		115					120					125				
tgg	gac	gag	gac	ggc	cac	cac	gca	cag	gat	tca	ctc	cac	tac	gaa	ggc	432
Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly	
	130					135					140					
cgt	gcc	ttg	gac	atc	acc	acg	tct	gac	cgt	gac	cgt	aat	aag	tat	ggt	480
Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly	
145					150					155					160	
ttg	ttg	gcg	cgc	cta	gct	gtg	gaa	gcc	gga	ttc	gac	tgg	gtc	tac	tac	528
Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	
				165					170					175		
gag	tcc	cgc	aac	cac	atc	cac	gta	tcg	gtc	aaa	gct	gat	aac	tca	ctg	576
Glu	Ser	Arg	Asn	His	Ile	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu	
			180					185					190			
gcg	gtc	cga	gcc	gga	ggc	tgc	ttt	ccg	gga	aat	gcc	acg	gtg	cgc	ttg	624
Ala	Val	Arg	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu	
		195					200					205				
cgg	agc	ggc	gaa	cgg	aag	ggg	ctg	agg	gaa	cta	cat	cgt	ggt	gac	tgg	672
Arg	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp	
	210					215					220					
gta	ctg	gcc	gct	gat	gca	gcg	ggc	cga	gtg	gta	ccc	acg	cca	gtg	ctg	720
Val	Leu	Ala	Ala	Asp	Ala	Ala	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu	
225					230					235					240	
ctc	ttc	ctg	gac	cgg	gat	ctg	cag	cgc	cgc	gcc	tcg	ttc	gtg	gct	gtg	768

a069seq

Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val		
				245					250					255			
gag acc gag cgg cct ccg cgc aaa ctg ttg ctc aca ccc tgg cat ctg																	816
Glu	Thr	Glu	Arg	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu		
			260					265					270				
gtg ttc gct gct cgc ggg cca gcg cct gct cca ggt gac ttt gca ccg																	864
Val	Phe	Ala	Ala	Arg	Gly	Pro	Ala	Pro	Ala	Pro	Gly	Asp	Phe	Ala	Pro		
		275					280					285					
gtg ttc gcg cgc cgc tta cgt gct ggc gac tcg gtg ctg gct ccc ggc																	912
Val	Phe	Ala	Arg	Arg	Leu	Arg	Ala	Gly	Asp	Ser	Val	Leu	Ala	Pro	Gly		
	290					295					300						
ggg gac gcg ctc cag ccg gcg cgc gta gcc cgc gtg gcg cgc gag gaa																	960
Gly	Asp	Ala	Leu	Gln	Pro	Ala	Arg	Val	Ala	Arg	Val	Ala	Arg	Glu	Glu		
305					310					315				320			
gcc gtg ggc gtg ttc gca ccg ctc act gcg cac ggg acg ctg ctg gtc																	1008
Ala	Val	Gly	Val	Phe	Ala	Pro	Leu	Thr	Ala	His	Gly	Thr	Leu	Leu	Val		
				325					330					335			
aac gac gtc ctc gcc tcc tgc tac gcg gtt cta gag agt cac cag tgg																	1056
Asn	Asp	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Leu	Glu	Ser	His	Gln	Trp		
			340					345					350				
gcc cac cgc gcc ttc gcc cct ttg cgg ctg ctg cac gcg ctc ggg gct																	1104
Ala	His	Arg	Ala	Phe	Ala	Pro	Leu	Arg	Leu	Leu	His	Ala	Leu	Gly	Ala		
		355					360					365					
ctg ctc cct ggg ggt gca gtc cag ccg act ggc atg cat tgg tac tct																	1152
Leu	Leu	Pro	Gly	Gly	Ala	Val	Gln	Pro	Thr	Gly	Met	His	Trp	Tyr	Ser		
	370					375					380						
cgc ctc ctt tac cgc ttg gcc gag gag tta atg ggc tg																	1190
Arg	Leu	Leu	Tyr	Arg	Leu	Ala	Glu	Glu	Leu	Met	Gly						
385					390					395							
<210> 3																	
<211> 1281																	
<212> DNA																	

a069seq

<213> Murine sp.

<220>

<221> CDS

<222> (1)..(1233)

<400> 3

```

atg tct ccc gcc tgg ctc cgg ccc cga ctg cgg ttc tgt ctg ttc ctg      48
Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu
  1           5           10           15

ctg ctg ctg ctt ctg gtg ccg gcg gcg cgg ggc tgc ggg ccg ggc cgg      96
Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
          20           25           30

gtg gtg ggc agc cgc cgg agg ccg cct cgc aag ctc gtg cct ctt gcc     144
Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
      35           40           45

tac aag cag ttc agc ccc aac gtg ccg gag aag acc ctg ggc gcc agc     192
Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
      50           55           60

ggg cgc tac gaa ggc aag atc gcg cgc agc tct gag cgc ttc aaa gag     240
Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
  65           70           75           80

ctc acc ccc aac tac aat ccc gac atc atc ttc aag gac gag gag aac     288
Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
          85           90           95

acg ggt gcc gac cgc ctc atg acc cag cgc tgc aag gac cgt ctg aac     336
Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
          100          105          110

tca ctg gcc atc tct gtc atg aac cag tgg cct ggt gtg aaa ctg cgg     384
Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
          115          120          125

gtg acc gaa ggc cgg gat gaa gat ggc cat cac tca gag gag tct tta     432
Val Thr Glu Gly Arg Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
  130           135           140

```

a069seq

cac tat gag ggc cgc gcg gtg gat atc acc acc tca gac cgt gac cga	480
His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg	
145 150 155 160	
aat aag tat gga ctg ctg gcg cgc tta gca gtg gag gcc ggc ttc gac	528
Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp	
165 170 175	
tgg gtg tat tac gag tcc aag gcc cac gtg cat tgc tct gtc aag tct	576
Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser	
180 185 190	
gag cat tcg gcc gct gcc aag aca ggt ggc tgc ttt cct gcc gga gcc	624
Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala	
195 200 205	
cag gtg cgc cta gag aac ggg gag cgt gtg gcc ctg tca gct gta aag	672
Gln Val Arg Leu Glu Asn Gly Glu Arg Val Ala Leu Ser Ala Val Lys	
210 215 220	
cca gga gac cgg gtg ctg gcc atg ggg gag gat ggg acc ccc acc ttc	720
Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Thr Pro Thr Phe	
225 230 235 240	
agt gat gtg ctt att ttc ctg gac cgc gag cca aac cgg ctg aga gct	768
Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro Asn Arg Leu Arg Ala	
245 250 255	
ttc cag gtc atc gag act cag gat cct ccg cgt cgg ctg gcg ctc acg	816
Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr	
260 265 270	
cct gcc cac ctg ctc ttc att gcg gac aat cat aca gaa cca gca gcc	864
Pro Ala His Leu Leu Phe Ile Ala Asp Asn His Thr Glu Pro Ala Ala	
275 280 285	
cac ttc cgg gcc aca ttt gcc agc cat gtg caa cca ggc caa tat gtg	912
His Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val	
290 295 300	

a069seq

```

ctg gta tca ggg gta cca ggc ctc cag cct gct cgg gtg gca gct gtc      960
Leu Val Ser Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val
305                      310                      315                      320

tcc acc cac gtg gcc ctt ggg tcc tat gct cct ctc aca agg cat ggg      1008
Ser Thr His Val Ala Leu Gly Ser Tyr Ala Pro Leu Thr Arg His Gly
                      325                      330                      335

aca ctt gtg gtg gag gat gtg gtg gcc tcc tgc ttt gca gct gtg gct      1056
Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala
                      340                      345                      350

gac cac cat ctg gct cag ttg gcc ttc tgg ccc ctg cga ctg ttt ccc      1104
Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe Pro
                      355                      360                      365

agt ttg gca tgg ggc agc tgg acc cca agt gag ggt gtt cac tcc tac      1152
Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr
                      370                      375                      380

cct cag atg ctc tac cgc ctg ggg cgt ctc ttg cta gaa gag agc acc      1200
Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Ser Thr
385                      390                      395                      400

ttc cat cca ctg ggc atg tct ggg gca gga agc tgaagggact ctaaccactg 1253
Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser
                      405                      410

ccctcctgga actgctgtgc gtggatcc                                     1281

```

<210> 4
 <211> 1313
 <212> DNA
 <213> Murine sp.

<220>
 <221> CDS
 <222> (1)..(1311)

<400> 4
 atg ctg ctg ctg ctg gcc aga tgt ttt ctg gtg atc ctt gct tcc tcg 48

a069seq

Met	Leu	Leu	Leu	Leu	Ala	Arg	Cys	Phe	Leu	Val	Ile	Leu	Ala	Ser	Ser		
1				5					10					15			
ctg	ctg	gtg	tgc	ccc	ggg	ctg	gcc	tgt	ggg	ccc	ggc	agg	ggg	ttt	gga	96	
Leu	Leu	Val	Cys	Pro	Gly	Leu	Ala	Cys	Gly	Pro	Gly	Arg	Gly	Phe	Gly		
			20					25					30				
aag	agg	cgg	cac	ccc	aaa	aag	ctg	acc	cct	tta	gcc	tac	aag	cag	ttt	144	
Lys	Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe		
		35					40					45					
att	ccc	aac	gta	gcc	gag	aag	acc	cta	ggg	gcc	agc	ggc	aga	tat	gaa	192	
Ile	Pro	Asn	Val	Ala	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	Tyr	Glu		
	50					55					60						
ggg	aag	atc	aca	aga	aac	tcc	gaa	cga	ttt	aag	gaa	ctc	acc	ccc	aat	240	
Gly	Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn		
65					70				75						80		
tac	aac	ccc	gac	atc	ata	ttt	aag	gat	gag	gaa	aac	acg	gga	gca	gac	288	
Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp		
				85				90						95			
cgg	ctg	atg	act	cag	agg	tgc	aaa	gac	aag	tta	aat	gcc	ttg	gcc	atc	336	
Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ala	Leu	Ala	Ile		
			100					105					110				
tct	gtg	atg	aac	cag	tgg	cct	gga	gtg	agg	ctg	cga	gtg	acc	gag	ggc	384	
Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly		
		115					120					125					
tgg	gat	gag	gac	ggc	cat	cat	tca	gag	gag	tct	cta	cac	tat	gag	ggt	432	
Trp	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly		
130						135					140						
cga	gca	gtg	gac	atc	acc	acg	tcc	gac	cgg	gac	cgc	agc	aag	tac	ggc	480	
Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Ser	Lys	Tyr	Gly		
145					150					155					160		
atg	ctg	gct	cgc	ctg	gct	gtg	gaa	gca	ggt	ttc	gac	tgg	gtc	tac	tat	528	
Met	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr		

															a069seq						
															165	170	175				
gaa tcc aaa gct cac atc cac tgt tct gtg aaa gca gag aac tcc gtg																					576
Glu	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	180	185	190			
gcg gcc aaa tcc ggc ggc tgt ttc ccg gga tcc gcc acc gtg cac ctg																					624
Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val	His	Leu	195	200	205			
gag cag ggc ggc acc aag ctg gtg aag gac tta cgt ccc gga gac cgc																					672
Glu	Gln	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Arg	210	215	220			
gtg ctg gcg gct gac gac cag ggc cgg ctg ctg tac agc gac ttc ctc																					720
Val	Leu	Ala	Ala	Asp	Asp	Gln	Gly	Arg	Leu	Leu	Tyr	Ser	Asp	Phe	Leu	225	230	235	240		
acc ttc ctg gac cgc gac gaa ggc gcc aag aag gtc ttc tac gtg atc																					768
Thr	Phe	Leu	Asp	Arg	Asp	Glu	Gly	Ala	Lys	Lys	Val	Phe	Tyr	Val	Ile	245	250	255			
gag acg ctg gag ccg cgc gag cgc ctg ctg ctc acc gcc gcg cac ctg																					816
Glu	Thr	Leu	Glu	Pro	Arg	Glu	Arg	Leu	Leu	Leu	Thr	Ala	Ala	His	Leu	260	265	270			
ctc ttc gtg gcg ccg cac aac gac tcg ggg ccc acg ccc ggg cca agc																					864
Leu	Phe	Val	Ala	Pro	His	Asn	Asp	Ser	Gly	Pro	Thr	Pro	Gly	Pro	Ser	275	280	285			
gcg ctc ttt gcc agc cgc gtg cgc ccc ggg cag cgc gtg tac gtg gtg																					912
Ala	Leu	Phe	Ala	Ser	Arg	Val	Arg	Pro	Gly	Gln	Arg	Val	Tyr	Val	Val	290	295	300			
gct gaa cgc ggc ggg gac cgc cgg ctg ctg ccc gcc gcg gtg cac agc																					960
Ala	Glu	Arg	Gly	Gly	Asp	Arg	Arg	Leu	Leu	Pro	Ala	Ala	Val	His	Ser	305	310	315	320		
gtg acg ctg cga gag gag gag gcg ggc gcg tac gcg ccg ctc acg gcg																					1008
Val	Thr	Leu	Arg	Glu	Glu	Glu	Ala	Gly	Ala	Tyr	Ala	Pro	Leu	Thr	Ala	325	330	335			

a069seq

```

cac ggc acc att ctc atc aac cgg gtg ctc gcc tcg tgc tac gct gtc      1056
His Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val
      340                      345                      350

atc gag gag cac agc tgg gca cac cgg gcc ttc gcg cct ttc cgc ctg      1104
Ile Glu Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu
      355                      360                      365

gcg cac gcg ctg ctg gcc gcg ctg gca ccc gcc cgc acg gac ggc ggg      1152
Ala His Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Gly Gly
      370                      375                      380

ggc ggg ggc agc atc cct gca gcg caa tct gca acg gaa gcg agg ggc      1200
Gly Gly Gly Ser Ile Pro Ala Ala Gln Ser Ala Thr Glu Ala Arg Gly
      385                      390                      395                      400

gcg gag ccg act gcg ggc atc cac tgg tac tcg cag ctg ctc tac cac      1248
Ala Glu Pro Thr Ala Gly Ile His Trp Tyr Ser Gln Leu Leu Tyr His
      405                      410                      415

att ggc acc tgg ctg ttg gac agc gag acc atg cat ccc ttg gga atg      1296
Ile Gly Thr Trp Leu Leu Asp Ser Glu Thr Met His Pro Leu Gly Met
      420                      425                      430

gcg gtc aag tcc agc tg                                          1313
Ala Val Lys Ser Ser
      435

<210> 5
<211> 1256
<212> DNA
<213> zebrafish sp.

<220>
<221> CDS
<222> (1)..(1254)

<400> 5
atg cgg ctt ttg acg aga gtg ctg ctg gtg tct ctt ctc act ctg tcc      48
Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser
      1                      5                      10                      15

```

a069seq

ttg	gtg	gtg	tcc	gga	ctg	gcc	tgc	ggg	cct	ggc	aga	ggc	tac	ggc	aga	96
Leu	Val	Val	Ser 20	Gly	Leu	Ala	Cys	Gly 25	Pro	Gly	Arg	Gly	Tyr 30	Gly	Arg	
aga	aga	cat	ccg	aag	aag	ctg	aca	cct	ctc	gcc	tac	aag	cag	ttc	ata	144
Arg	Arg	His 35	Pro	Lys	Lys	Leu	Thr 40	Pro	Leu	Ala	Tyr	Lys 45	Gln	Phe	Ile	
cct	aat	gtc	gcg	gag	aag	acc	tta	ggg	gcc	agc	ggc	aga	tac	gag	ggc	192
Pro	Asn 50	Val	Ala	Glu	Lys	Thr 55	Leu	Gly	Ala	Ser	Gly 60	Arg	Tyr	Glu	Gly	
aag	ata	acg	cgc	aat	tcg	gag	aga	ttt	aaa	gaa	ctt	act	cca	aat	tac	240
Lys 65	Ile	Thr	Arg	Asn	Ser 70	Glu	Arg	Phe	Lys	Glu 75	Leu	Thr	Pro	Asn	Tyr 80	
aat	ccc	gac	att	atc	ttt	aag	gat	gag	gag	aac	acg	gga	gcg	gac	agg	288
Asn	Pro	Asp	Ile	Ile 85	Phe	Lys	Asp	Glu	Glu 90	Asn	Thr	Gly	Ala	Asp 95	Arg	
ctc	atg	aca	cag	aga	tgc	aaa	gac	aag	ctg	aac	tcg	ctg	gcc	atc	tct	336
Leu	Met	Thr	Gln 100	Arg	Cys	Lys	Asp	Lys 105	Leu	Asn	Ser	Leu	Ala 110	Ile	Ser	
gta	atg	aac	cac	tgg	cca	ggg	gtt	aag	ctg	cgt	gtg	aca	gag	ggc	tgg	384
Val	Met	Asn 115	His	Trp	Pro	Gly	Val 120	Lys	Leu	Arg	Val	Thr 125	Glu	Gly	Trp	
gat	gag	gac	ggg	cac	cat	ttt	gaa	gaa	tca	ctc	cac	tac	gag	gga	aga	432
Asp	Glu 130	Asp	Gly	His	His	Phe 135	Glu	Glu	Ser	Leu	His 140	Tyr	Glu	Gly	Arg	
gct	gtt	gat	att	acc	acc	tct	gac	cga	gac	aag	agc	aaa	tac	ggg	aca	480
Ala 145	Val	Asp	Ile	Thr	Thr 150	Ser	Asp	Arg	Asp	Lys 155	Ser	Lys	Tyr	Gly	Thr 160	
ctg	tct	cgc	cta	gct	gtg	gag	gct	gga	ttt	gac	tgg	gtc	tat	tac	gag	528
Leu	Ser	Arg	Leu	Ala 165	Val	Glu	Ala	Gly	Phe 170	Asp	Trp	Val	Tyr	Tyr 175	Glu	
tcc	aaa	gcc	cac	att	cat	tgc	tct	gtc	aaa	gca	gaa	aat	tcg	gtt	gct	576

a069seq

Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	Ala		
			180					185					190				
gcg	aaa	tct	ggg	ggc	tgt	ttc	cca	ggt	tcg	gct	ctg	gtc	tcg	ctc	cag	624	
Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Leu	Val	Ser	Leu	Gln		
		195					200					205					
gac	gga	gga	cag	aag	gcc	gtg	aag	gac	ctg	aac	ccc	gga	gac	aag	gtg	672	
Asp	Gly	Gly	Gln	Lys	Ala	Val	Lys	Asp	Leu	Asn	Pro	Gly	Asp	Lys	Val		
	210					215				220							
ctg	gcg	gca	gac	agc	gcg	gga	aac	ctg	gtg	ttc	agc	gac	ttc	atc	atg	720	
Leu	Ala	Ala	Asp	Ser	Ala	Gly	Asn	Leu	Val	Phe	Ser	Asp	Phe	Ile	Met		
225					230					235					240		
ttc	aca	gac	cga	gac	tcc	acg	acg	cga	cgt	gtg	ttt	tac	gtc	ata	gaa	768	
Phe	Thr	Asp	Arg	Asp	Ser	Thr	Thr	Arg	Arg	Val	Phe	Tyr	Val	Ile	Glu		
				245					250					255			
acg	caa	gaa	ccc	ggt	gaa	aag	atc	acc	ctc	acc	gcc	gct	cac	ctc	ctt	816	
Thr	Gln	Glu	Pro	Val	Glu	Lys	Ile	Thr	Leu	Thr	Ala	Ala	His	Leu	Leu		
			260					265					270				
ttt	gtc	ctc	gac	aac	tca	acg	gaa	gat	ctc	cac	acc	atg	acc	gcc	gcg	864	
Phe	Val	Leu	Asp	Asn	Ser	Thr	Glu	Asp	Leu	His	Thr	Met	Thr	Ala	Ala		
		275					280					285					
tat	gcc	agc	agt	gtc	aga	gcc	gga	caa	aag	gtg	atg	ggt	ggt	gat	gat	912	
Tyr	Ala	Ser	Ser	Val	Arg	Ala	Gly	Gln	Lys	Val	Met	Val	Val	Asp	Asp		
	290					295					300						
agc	ggt	cag	ctt	aaa	tct	gtc	atc	gtg	cag	cgg	ata	tac	acg	gag	gag	960	
Ser	Gly	Gln	Leu	Lys	Ser	Val	Ile	Val	Gln	Arg	Ile	Tyr	Thr	Glu	Glu		
305					310					315				320			
cag	cgg	ggc	tcg	ttc	gca	cca	gtg	act	gca	cat	ggg	acc	att	gtg	gtc	1008	
Gln	Arg	Gly	Ser	Phe	Ala	Pro	Val	Thr	Ala	His	Gly	Thr	Ile	Val	Val		
				325					330					335			
gac	aga	ata	ctg	gcg	tcc	tgt	tac	gcc	gta	ata	gag	gac	cag	ggg	ctt	1056	

a069seq

Asp	Arg	Ile	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Ile	Glu	Asp	Gln	Gly	Leu		
			340					345					350				
gcg	cat	ttg	gcc	ttc	gcg	ccc	gcc	agg	ctc	tat	tat	tac	gtg	tca	tca	1104	
Ala	His	Leu	Ala	Phe	Ala	Pro	Ala	Arg	Leu	Tyr	Tyr	Tyr	Val	Ser	Ser		
		355					360					365					
ttc	ctg	tcc	ccc	aaa	act	cca	gca	gtc	ggg	cca	atg	cga	ctt	tac	aac	1152	
Phe	Leu	Ser	Pro	Lys	Thr	Pro	Ala	Val	Gly	Pro	Met	Arg	Leu	Tyr	Asn		
	370					375					380						
agg	agg	ggg	tcc	act	ggg	act	cca	ggc	tcc	tgt	cat	caa	atg	gga	acg	1200	
Arg	Arg	Gly	Ser	Thr	Gly	Thr	Pro	Gly	Ser	Cys	His	Gln	Met	Gly	Thr		
385					390					395					400		
tgg	ctt	ttg	gac	agc	aac	atg	ctt	cat	cct	ttg	ggg	atg	tca	gta	aac	1248	
Trp	Leu	Leu	Asp	Ser	Asn	Met	Leu	His	Pro	Leu	Gly	Met	Ser	Val	Asn		
			405						410					415			
tca	agc	tg														1256	

Ser Ser

<210> 6

<211> 1425

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1425)

<220>

<223> "nnn" encoding "Xaa" at position 1387-1389 may be a, t, c, g, other or unknown

<400> 6

atg	ctg	ctg	ctg	gcg	aga	tgt	ctg	ctg	cta	gtc	ctc	gtc	tcc	tcg	ctg	48	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----	--

Met	Leu	Leu	Leu	Ala	Arg	Cys	Leu	Leu	Leu	Val	Leu	Val	Ser	Ser	Leu		
1				5					10					15			

ctg	gta	tgc	tcg	gga	ctg	gcg	tgc	gga	ccg	ggc	agg	ggg	ttc	ggg	aag	96	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----	--

Leu	Val	Cys	Ser	Gly	Leu	Ala	Cys	Gly	Pro	Gly	Arg	Gly	Phe	Gly	Lys		
			20					25					30				

a069seq

agg	agg	cac	ccc	aaa	aag	ctg	acc	cct	tta	gcc	tac	aag	cag	ttt	atc	144
Arg	Arg	His 35	Pro	Lys	Lys	Leu	Thr 40	Pro	Leu	Ala	Tyr	Lys 45	Gln	Phe	Ile	
ccc	aat	gtg	gcc	gag	aag	acc	cta	ggc	gcc	agc	gga	agg	tat	gaa	ggg	192
Pro	Asn 50	Val	Ala	Glu	Lys	Thr 55	Leu	Gly	Ala	Ser	Gly 60	Arg	Tyr	Glu	Gly	
aag	atc	tcc	aga	aac	tcc	gag	cga	ttt	aag	gaa	ctc	acc	ccc	aat	tac	240
Lys 65	Ile	Ser	Arg	Asn	Ser 70	Glu	Arg	Phe	Lys	Glu 75	Leu	Thr	Pro	Asn	Tyr 80	
aac	ccc	gac	atc	ata	ttt	aag	gat	gaa	gaa	aac	acc	gga	gcg	gac	agg	288
Asn	Pro	Asp	Ile	Ile 85	Phe	Lys	Asp	Glu	Glu 90	Asn	Thr	Gly	Ala	Asp 95	Arg	
ctg	atg	act	cag	agg	tgt	aag	gac	aag	ttg	aac	gct	ttg	gcc	atc	tcg	336
Leu	Met	Thr 100	Gln	Arg	Cys	Lys	Asp	Lys 105	Leu	Asn	Ala	Leu	Ala 110	Ile	Ser	
gtg	atg	aac	cag	tgg	cca	gga	gtg	aaa	ctg	cgg	gtg	acc	gag	ggc	tgg	384
Val	Met	Asn 115	Gln	Trp	Pro	Gly	Val 120	Lys	Leu	Arg	Val	Thr 125	Glu	Gly	Trp	
gac	gaa	gat	ggc	cac	cac	tca	gag	gag	tct	ctg	cac	tac	gag	ggc	cgc	432
Asp 130	Glu	Asp	Gly	His	His	Ser 135	Glu	Glu	Ser	Leu	His 140	Tyr	Glu	Gly	Arg	
gca	gtg	gac	atc	acc	acg	tct	gac	cgc	gac	cgc	agc	aag	tac	ggc	atg	480
Ala 145	Val	Asp	Ile	Thr	Thr 150	Ser	Asp	Arg	Asp	Arg 155	Ser	Lys	Tyr	Gly	Met 160	
ctg	gcc	cgc	ctg	gcg	gtg	gag	gcc	ggc	ttc	gac	tgg	gtg	tac	tac	gag	528
Leu	Ala	Arg	Leu	Ala 165	Val	Glu	Ala	Gly	Phe 170	Asp	Trp	Val	Tyr	Tyr 175	Glu	
tcc	aag	gca	cat	atc	cac	tgc	tcg	gtg	aaa	gca	gag	aac	tcg	gtg	gcg	576
Ser	Lys	Ala	His 180	Ile	His	Cys	Ser	Val 185	Lys	Ala	Glu	Asn	Ser 190	Val	Ala	
gcc	aaa	tcg	gga	ggc	tgc	ttc	ccg	ggc	tcg	gcc	acg	gtg	cac	ctg	gag	624

a069seq

Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val	His	Leu	Glu	
		195					200					205				
cag	ggc	ggc	acc	aag	ctg	gtg	aag	gac	ctg	agc	ccc	ggg	gac	cgc	gtg	672
Gln	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Ser	Pro	Gly	Asp	Arg	Val	
	210					215					220					
ctg	gcg	gcg	gac	gac	cag	ggc	cgg	ctg	ctc	tac	agc	gac	ttc	ctc	act	720
Leu	Ala	Ala	Asp	Asp	Gln	Gly	Arg	Leu	Leu	Tyr	Ser	Asp	Phe	Leu	Thr	
225					230					235					240	
ttc	ctg	gac	cgc	gac	gac	ggc	gcc	aag	aag	gtc	ttc	tac	gtg	atc	gag	768
Phe	Leu	Asp	Arg	Asp	Asp	Gly	Ala	Lys	Lys	Val	Phe	Tyr	Val	Ile	Glu	
				245					250					255		
acg	cgg	gag	ccg	cgc	gag	cgc	ctg	ctg	ctc	acc	gcc	gcg	cac	ctg	ctc	816
Thr	Arg	Glu	Pro	Arg	Glu	Arg	Leu	Leu	Leu	Thr	Ala	Ala	His	Leu	Leu	
			260					265					270			
ttt	gtg	gcg	ccg	cac	aac	gac	tcg	gcc	acc	ggg	gag	ccc	gag	gcg	tcc	864
Phe	Val	Ala	Pro	His	Asn	Asp	Ser	Ala	Thr	Gly	Glu	Pro	Glu	Ala	Ser	
		275					280					285				
tcg	ggc	tcg	ggg	ccg	cct	tcc	ggg	ggc	gca	ctg	ggg	cct	cgg	gcg	ctg	912
Ser	Gly	Ser	Gly	Pro	Pro	Ser	Gly	Gly	Ala	Leu	Gly	Pro	Arg	Ala	Leu	
	290					295					300					
ttc	gcc	agc	cgc	gtg	cgc	ccg	ggc	cag	cgc	gtg	tac	gtg	gtg	gcc	gag	960
Phe	Ala	Ser	Arg	Val	Arg	Pro	Gly	Gln	Arg	Val	Tyr	Val	Val	Ala	Glu	
305					310					315					320	
cgt	gac	ggg	gac	cgc	cgg	ctc	ctg	ccc	gcc	gct	gtg	cac	agc	gtg	acc	1008
Arg	Asp	Gly	Asp	Arg	Arg	Leu	Leu	Pro	Ala	Ala	Val	His	Ser	Val	Thr	
				325					330					335		
cta	agc	gag	gag	gcc	gcg	ggc	gcc	tac	gcg	ccg	ctc	acg	gcc	cag	ggc	1056
Leu	Ser	Glu	Glu	Ala	Ala	Gly	Ala	Tyr	Ala	Pro	Leu	Thr	Ala	Gln	Gly	
			340					345					350			
acc	att	ctc	atc	aac	cgg	gtg	ctg	gcc	tcg	tgc	tac	gcg	gtc	atc	gag	1104

a069seq

Thr	Ile	Leu	Ile	Asn	Arg	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Ile	Glu		
		355					360					365					
gag cac agc tgg gcg cac cgg gcc ttc gcg ccc ttc cgc ctg gcg cac 1152																	
Glu	His	Ser	Trp	Ala	His	Arg	Ala	Phe	Ala	Pro	Phe	Arg	Leu	Ala	His		
	370					375					380						
gcg ctc ctg gct gca ctg gcg ccc gcg cgc acg gac cgc ggc ggg gac 1200																	
Ala	Leu	Leu	Ala	Ala	Leu	Ala	Pro	Ala	Arg	Thr	Asp	Arg	Gly	Gly	Asp		
385					390					395					400		
agc ggc ggc ggg gac cgc ggg ggc ggc ggc ggc aga gta gcc cta acc 1248																	
Ser	Gly	Gly	Gly	Asp	Arg	Gly	Gly	Gly	Gly	Gly	Arg	Val	Ala	Leu	Thr		
				405					410					415			
gct cca ggt gct gcc gac gct ccg ggt gcg ggg gcc acc gcg ggc atc 1296																	
Ala	Pro	Gly	Ala	Ala	Asp	Ala	Pro	Gly	Ala	Gly	Ala	Thr	Ala	Gly	Ile		
			420					425					430				
cac tgg tac tcg cag ctg ctc tac caa ata ggc acc tgg ctc ctg gac 1344																	
His	Trp	Tyr	Ser	Gln	Leu	Leu	Tyr	Gln	Ile	Gly	Thr	Trp	Leu	Leu	Asp		
		435					440					445					
agc gag gcc ctg cac ccg ctg ggc atg gcg gtc aag tcc agc nnn agc 1392																	
Ser	Glu	Ala	Leu	His	Pro	Leu	Gly	Met	Ala	Val	Lys	Ser	Ser	Xaa	Ser		
	450					455					460						
cgg ggg gcc ggg gga ggg gcg cgg gag ggg gcc 1425																	
Arg	Gly	Ala	Gly	Gly	Gly	Ala	Arg	Glu	Gly	Ala							
465					470					475							
<210> 7																	
<211> 1622																	
<212> DNA																	
<213> Homo sapiens																	
<220>																	
<221> CDS																	
<222> (51)..(1283)																	
<400> 7																	
catcagccca ccaggagacc tcgcccgcgc ctcccccgagg ctcccccggcc atg tct 56																	

Met Ser

a069seq

1

```

ccc gcc cgg ctc cgg ccc cga ctg cac ttc tgc ctg gtc ctg ttg ctg      104
Pro Ala Arg Leu Arg Pro Arg Leu His Phe Cys Leu Val Leu Leu Leu
      5              10              15

ctg ctg gtg gtg ccc gcg gca tgg ggc tgc ggg ccg ggt cgg gtg gtg      152
Leu Leu Val Val Pro Ala Ala Trp Gly Cys Gly Pro Gly Arg Val Val
      20              25              30

ggc agc cgc cgg cga ccg cca cgc aaa ctc gtg ccg ctc gcc tac aag      200
Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala Tyr Lys
      35              40              45              50

cag ttc agc ccc aat gtg ccc gag aag acc ctg ggc gcc agc gga cgc      248
Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser Gly Arg
      55              60              65

tat gaa ggc aag atc gct cgc agc tcc gag cgc ttc aag gag ctc acc      296
Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu Leu Thr
      70              75              80

ccc aat tac aat cca gac atc atc ttc aag gac gag gag aac aca ggc      344
Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly
      85              90              95

gcc gac cgc ctc atg acc cag cgc tgc aag gac cgc ctg aac tcg ctg      392
Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn Ser Leu
      100              105              110

gct atc tcg gtg atg aac cag tgg ccc ggt gtg aag ctg cgg gtg acc      440
Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr
      115              120              125              130

gag ggc tgg gac gag gac ggc cac cac tca gag gag tcc ctg cat tat      488
Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr
      135              140              145

gag ggc cgc gcg gtg gac atc acc aca tca gac cgc gac cgc aat aag      536
Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys
      150              155              160

```

a069seq

tat gga ctg ctg gcg cgc ttg gca gtg gag gcc ggc ttt gac tgg gtg	584
Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val	
165 170 175	
tat tac gag tca aag gcc cac gtg cat tgc tcc gtc aag tcc gag cac	632
Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser Glu His	
180 185 190	
tcg gcc gca gcc aag acg ggc ggc tgc ttc cct gcc gga gcc cag gta	680
Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala Gln Val	
195 200 205 210	
cgc ctg gag agt ggg gcg cgt gtg gcc ttg tca gcc gtg agg ccg gga	728
Arg Leu Glu Ser Gly Ala Arg Val Ala Leu Ser Ala Val Arg Pro Gly	
215 220 225	
gac cgt gtg ctg gcc atg ggg gag gat ggg agc ccc acc ttc agc gat	776
Asp Arg Val Leu Ala Met Gly Glu Asp Gly Ser Pro Thr Phe Ser Asp	
230 235 240	
gtg ctc att ttc ctg gac cgc gag ccc cac agg ctg aga gcc ttc cag	824
Val Leu Ile Phe Leu Asp Arg Glu Pro His Arg Leu Arg Ala Phe Gln	
245 250 255	
gtc atc gag act cag gac ccc cca cgc cgc ctg gca ctc aca ccc gct	872
Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr Pro Ala	
260 265 270	
cac ctg ctc ttt acg gct gac aat cac acg gag ccg gca gcc cgc ttc	920
His Leu Leu Phe Thr Ala Asp Asn His Thr Glu Pro Ala Ala Arg Phe	
275 280 285 290	
cgg gcc aca ttt gcc agc cac gtg cag cct ggc cag tac gtg ctg gtg	968
Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val Leu Val	
295 300 305	
gct ggg gtg cca ggc ctg cag cct gcc cgc gtg gca gct gtc tct aca	1016
Ala Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val Ser Thr	
310 315 320	

a069seq

```

cac gtg gcc ctc ggg gcc tac gcc ccg ctc aca aag cat ggg aca ctg      1064
His Val Ala Leu Gly Ala Tyr Ala Pro Leu Thr Lys His Gly Thr Leu
      325                      330                      335

gtg gtg gag gat gtg gtg gca tcc tgc ttc gcg gcc gtg gct gac cac      1112
Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala Asp His
      340                      345                      350

cac ctg gct cag ttg gcc ttc tgg ccc ctg aga ctc ttt cac agc ttg      1160
His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe His Ser Leu
      355                      360                      365                      370

gca tgg ggc agc tgg acc ccg ggg gag ggt gtg cat tgg tac ccc cag      1208
Ala Trp Gly Ser Trp Thr Pro Gly Glu Gly Val His Trp Tyr Pro Gln
      375                      380                      385

ctg ctc tac cgc ctg ggg cgt ctc ctg cta gaa gag ggc agc ttc cac      1256
Leu Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Gly Ser Phe His
      390                      395                      400

cca ctg ggc atg tcc ggg gca ggg agc tgaaaggact ccaccgctgc      1303
Pro Leu Gly Met Ser Gly Ala Gly Ser
      405                      410

cctcctggaa ctgctgtact ggggtccagaa gcctctcagc caggagggag ctggccctgg 1363

aagggaacctg agctggggga cactgggtcc tgccatctcc tctgcatga agatacacca 1423

ttgagacttg actgggcaac accagcgtcc cccacccgcg tcgtaggtgta gtcatagagc 1483

tgcaagctga gctggcgagg ggatgggtgt tgacccctct ctctagaga ccttgaggct 1543

ggcacggcga ctcccaactc agcctgctct cactacgagt tttcatactc tgcctcccc 1603

attgggaggg ccattccc      1622

```

<210> 8
 <211> 1190
 <212> DNA

a069seq

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1188)

<400> 8

```

atg gct ctc ctg acc aat cta ctg ccc ttg tgc tgc ttg gca ctt ctg      48
Met Ala Leu Leu Thr Asn Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
  1              5              10              15

gcg ctg cca gcc cag agc tgc ggg ccg ggc cgg ggg ccg gtt ggc cgg      96
Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
      20              25              30

cgc cgc tat gcg cgc aag cag ctc gtg ccg cta ctc tac aag caa ttt     144
Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
      35              40              45

gtg ccc ggc gtg cca gag cgg acc ctg ggc gcc agt ggg cca gcg gag     192
Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
      50              55              60

ggg agg gtg gca agg ggc tcc gag cgc ttc cgg gac ctc gtg ccc aac     240
Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
      65              70              75              80

tac aac ccc gac atc atc ttc aag gat gag gag aac agt gga gcc gac     288
Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
      85              90              95

cgc ctg atg acc gag cgt tgc aag gag agg gtg aac gct ttg gcc att     336
Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
      100              105              110

gcc gtg atg aac atg tgg ccc gga gtg cgc cta cga gtg act gag ggc     384
Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
      115              120              125

tgg gac gag gac ggc cac cac gct cag gat tca ctc cac tac gaa ggc     432
Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
      130              135              140

```

a069seq

```

cgt gct ttg gac atc act acg tct gac cgc gac cgc aac aag tat ggg      480
Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
145                               150                               155                               160

ttg ctg gcg cgc ctc gca gtg gaa gcc ggc ttc gac tgg gtc tac tac      528
Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
                               165                               170                               175

gag tcc cgc aac cac gtc cac gtg tcg gtc aaa gct gat aac tca ctg      576
Glu Ser Arg Asn His Val His Val Ser Val Lys Ala Asp Asn Ser Leu
                               180                               185                               190

gcg gtc cgg gcg ggc ggc tgc ttt ccg gga aat gca act gtg cgc ctg      624
Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu
                               195                               200                               205

tgg agc ggc gag cgg aaa ggg ctg cgg gaa ctg cac cgc gga gac tgg      672
Trp Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp
210                               215                               220

gtt ttg gcg gcc gat gcg tca ggc cgg gtg gtg ccc acg ccg gtg ctg      720
Val Leu Ala Ala Asp Ala Ser Gly Arg Val Val Pro Thr Pro Val Leu
225                               230                               235

ctc ttc ctg gac cgg gac ttg cag cgc cgg gct tca ttt gtg gct gtg      768
Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val
                               245                               250                               255

gag acc gag tgg cct cca cgc aaa ctg ttg ctc acg ccc tgg cac ctg      816
Glu Thr Glu Trp Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu
                               260                               265                               270

gtg ttt gcc gct cga ggg ccg gcg ccc gcg cca ggc gac ttt gca ccg      864
Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro
                               275                               280                               285

gtg ttc gcg cgc cgg cta cgc gct ggg gac tcg gtg ctg gcg ccc ggc      912
Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
290                               295                               300

```

a069seq

```

ggg gat gcg ctt cgg cca gcg cgc gtg gcc cgt gtg gcg cgg gag gaa 960
Gly Asp Ala Leu Arg Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
305          310          315          320

gcc gtg ggc gtg ttc gcg ccg ctc acc gcg cac ggg acg ctg ctg gtg 1008
Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
          325          330          335

aac gat gtc ctg gcc tct tgc tac gcg gtt ctg gag agt cac cag tgg 1056
Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
          340          345          350

gcg cac cgc gct ttt gcc ccc ttg aga ctg ctg cac gcg cta ggg gcg 1104
Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
          355          360          365

ctg ctc ccc ggc ggg gcc gtc cag ccg act ggc atg cat tgg tac tct 1152
Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
          370          375          380

cgg ctc ctc tac cgc tta gcg gag gag cta ctg ggc tg 1190
Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly
385          390          395

<210> 9
<211> 1251
<212> DNA
<213> Zebrafish sp.

<220>
<221> CDS
<222> (1)..(1248)

<400> 9
atg gac gta agg ctg cat ctg aag caa ttt gct tta ctg tgt ttt atc 48
Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile
 1          5          10          15

agc ttg ctt ctg acg cct tgt gga tta gcc tgt ggt cct ggt aga ggt 96
Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly
          20          25          30

tat gga aaa cga aga cac cca aag aaa tta acc ccg ttg gct tac aag 144

```


a069seq

Tyr	Gly	Lys	Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys		
		35					40					45					
caa	ttc	atc	ccc	aac	gtt	gct	gag	aaa	acg	ctt	gga	gcc	agc	ggc	aaa	192	
Gln	Phe	Ile	Pro	Asn	Val	Ala	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Lys		
	50					55					60						
tac	gaa	ggc	aaa	atc	aca	agg	aat	tca	gag	aga	ttt	aaa	gag	ctg	att	240	
Tyr	Glu	Gly	Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Ile		
65					70					75					80		
ccg	aat	tat	aat	ccc	gat	atc	atc	ttt	aag	gac	gag	gaa	aac	aca	aac	288	
Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Asn		
				85					90					95			
gct	gac	agg	ctg	atg	acc	aag	cgc	tgt	aag	gac	aag	tta	aat	tcg	ttg	336	
Ala	Asp	Arg	Leu	Met	Thr	Lys	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ser	Leu		
			100					105					110				
gcc	ata	tcc	gtc	atg	aac	cac	tgg	ccc	ggc	gtg	aaa	ctg	cgc	gtc	act	384	
Ala	Ile	Ser	Val	Met	Asn	His	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr		
		115					120					125					
gaa	ggc	tgg	gat	gag	gat	ggt	cac	cat	tta	gaa	gaa	tct	ttg	cac	tat	432	
Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	Leu	Glu	Glu	Ser	Leu	His	Tyr		
	130					135					140						
gag	gga	cgg	gca	gtg	gac	atc	act	acc	tca	gac	agg	gat	aaa	agc	aag	480	
Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Lys	Ser	Lys		
145					150					155					160		
tat	ggg	atg	cta	tcc	agg	ctt	gca	gtg	gag	gca	gga	ttc	gac	tgg	gtc	528	
Tyr	Gly	Met	Leu	Ser	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val		
				165					170					175			
tat	tat	gaa	tct	aaa	gcc	cac	ata	cac	tgc	tct	gtc	aaa	gca	gaa	aat	576	
Tyr	Tyr	Glu	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn		
			180					185					190				
tca	gtg	gct	gct	aaa	tca	gga	gga	tgt	ttt	cct	ggg	tct	ggg	acg	gtg	624	

a069seq

Ser	Val	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Gly	Thr	Val		
		195					200					205					
aca	ctt	ggt	gat	ggg	acg	agg	aaa	ccc	atc	aaa	gat	ctt	aaa	gtg	ggc	672	
Thr	Leu	Gly	Asp	Gly	Thr	Arg	Lys	Pro	Ile	Lys	Asp	Leu	Lys	Val	Gly		
	210					215					220						
gac	cgg	ggt	ttg	gct	gca	gac	gag	aag	gga	aat	gtc	tta	ata	agc	gac	720	
Asp	Arg	Val	Leu	Ala	Ala	Asp	Glu	Lys	Gly	Asn	Val	Leu	Ile	Ser	Asp		
225					230					235					240		
ttt	att	atg	ttt	ata	gac	cac	gat	ccg	aca	acg	aga	agg	caa	ttc	atc	768	
Phe	Ile	Met	Phe	Ile	Asp	His	Asp	Pro	Thr	Thr	Arg	Arg	Gln	Phe	Ile		
				245					250					255			
gtc	atc	gag	acg	tca	gaa	cct	ttc	acc	aag	ctc	acc	ctc	act	gcc	gcg	816	
Val	Ile	Glu	Thr	Ser	Glu	Pro	Phe	Thr	Lys	Leu	Thr	Leu	Thr	Ala	Ala		
			260					265					270				
cac	cta	ggt	ttc	ggt	gga	aac	tct	tca	gca	gct	tcg	ggt	ata	aca	gca	864	
His	Leu	Val	Phe	Val	Gly	Asn	Ser	Ser	Ala	Ala	Ser	Gly	Ile	Thr	Ala		
		275					280					285					
aca	ttt	gcc	agc	aac	gtg	aag	cct	gga	gat	aca	ggt	tta	gtg	tgg	gaa	912	
Thr	Phe	Ala	Ser	Asn	Val	Lys	Pro	Gly	Asp	Thr	Val	Leu	Val	Trp	Glu		
	290					295					300						
gac	aca	tgc	gag	agc	ctc	aag	agc	ggt	aca	gtg	aaa	agg	att	tac	act	960	
Asp	Thr	Cys	Glu	Ser	Leu	Lys	Ser	Val	Thr	Val	Lys	Arg	Ile	Tyr	Thr		
305					310					315					320		
gag	gag	cac	gag	ggc	tct	ttt	gcg	cca	gtc	acc	gcg	cac	gga	acc	ata	1008	
Glu	Glu	His	Glu	Gly	Ser	Phe	Ala	Pro	Val	Thr	Ala	His	Gly	Thr	Ile		
				325					330				335				
ata	gtg	gat	cag	gtg	ttg	gca	tcg	tgc	tac	gcg	gtc	att	gag	aac	cac	1056	
Ile	Val	Asp	Gln	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Ile	Glu	Asn	His		
			340					345					350				
aaa	tgg	gca	cat	tgg	gct	ttt	gcg	ccg	gtc	agg	ttg	tgt	cac	aag	ctg	1104	
Lys	Trp	Ala	His	Trp	Ala	Phe	Ala	Pro	Val	Arg	Leu	Cys	His	Lys	Leu		

)

)

a069seq

355

360

365

atg acg tgg ctt ttt ccg gct cgt gaa tca aac gtc aat ttt cag gag 1152

Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu
370 375 380

gat ggt atc cac tgg tac tca aat atg ctg ttt cac atc ggc tct tgg 1200

Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp
385 390 395 400

ctg ctg gac aga gac tct ttc cat cca ctc ggg att tta cac tta agt 1248

Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser
405 410 415

tga 1251

<210> 10

<211> 425

<212> PRT

<213> Gallus sp.

<400> 10

Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile
1 5 10 15

Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly
20 25 30

Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
35 40 45

Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg
50 55 60

Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr
65 70 75 80

Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly
85 90 95

Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu
100 105 110

Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr
115 120 125

Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr

a069seq

130						135						140					
Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Ser	Lys		
145					150					155					160		
Tyr	Gly	Met	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val		
				165					170					175			
Tyr	Tyr	Glu	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn		
			180					185					190				
Ser	Val	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val		
		195					200					205					
His	Leu	Glu	His	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Ser	Pro	Gly		
	210					215					220						
Asp	Arg	Val	Leu	Ala	Ala	Asp	Ala	Asp	Gly	Arg	Leu	Leu	Tyr	Ser	Asp		
225					230					235					240		
Phe	Leu	Thr	Phe	Leu	Asp	Arg	Met	Asp	Ser	Ser	Arg	Lys	Leu	Phe	Tyr		
				245					250					255			
Val	Ile	Glu	Thr	Arg	Gln	Pro	Arg	Ala	Arg	Leu	Leu	Leu	Thr	Ala	Ala		
			260					265					270				
His	Leu	Leu	Phe	Val	Ala	Pro	Gln	His	Asn	Gln	Ser	Glu	Ala	Thr	Gly		
		275					280					285					
Ser	Thr	Ser	Gly	Gln	Ala	Leu	Phe	Ala	Ser	Asn	Val	Lys	Pro	Gly	Gln		
	290					295					300						
Arg	Val	Tyr	Val	Leu	Gly	Glu	Gly	Gly	Gln	Gln	Leu	Leu	Pro	Ala	Ser		
305					310					315					320		
Val	His	Ser	Val	Ser	Leu	Arg	Glu	Glu	Ala	Ser	Gly	Ala	Tyr	Ala	Pro		
				325					330					335			
Leu	Thr	Ala	Gln	Gly	Thr	Ile	Leu	Ile	Asn	Arg	Val	Leu	Ala	Ser	Cys		
			340					345					350				
Tyr	Ala	Val	Ile	Glu	Glu	His	Ser	Trp	Ala	His	Trp	Ala	Phe	Ala	Pro		
		355					360					365					
Phe	Arg	Leu	Ala	Gln	Gly	Leu	Leu	Ala	Ala	Leu	Cys	Pro	Asp	Gly	Ala		
	370					375					380						
Ile	Pro	Thr	Ala	Ala	Thr	Thr	Thr	Thr	Gly	Ile	His	Trp	Tyr	Ser	Arg		
385					390					395					400		
Leu	Leu	Tyr	Arg	Ile	Gly	Ser	Trp	Val	Leu	Asp	Gly	Asp	Ala	Leu	His		

a069seq
410

405

415

Pro Leu Gly Met Val Ala Pro Ala Ser
420 425

<210> 11
<211> 396
<212> PRT
<213> Murine sp.

<400> 11

Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
1 5 10 15
Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
20 25 30
Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
35 40 45
Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
50 55 60
Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
65 70 75 80
Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
85 90 95
Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
100 105 110
Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
115 120 125
Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
130 135 140
Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
145 150 155 160
Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
165 170 175
Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu
180 185 190
Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu
195 200 205
Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp

a069seq

210

215

220

Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu
225 230 235 240

Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val
245 250 255

Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu
260 265 270

Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro
275 280 285

Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
290 295 300

Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
305 310 315 320

Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
325 330 335

Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
340 345 350

Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
355 360 365

Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
370 375 380

Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly
385 390 395

<210> 12

<211> 411

<212> PRT

<213> Murine sp.

<400> 12

Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu
1 5 10 15

Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
20 25 30

Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
35 40 45

Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser

a069seq

50					55					60					
Gly	Arg	Tyr	Glu	Gly	Lys	Ile	Ala	Arg	Ser	Ser	Glu	Arg	Phe	Lys	Glu
65					70					75					80
Leu	Thr	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn
				85					90					95	
Thr	Gly	Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Arg	Leu	Asn
			100					105					110		
Ser	Leu	Ala	Ile	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg
		115					120					125			
Val	Thr	Glu	Gly	Arg	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu
		130				135					140				
His	Tyr	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg
145					150					155					160
Asn	Lys	Tyr	Gly	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp
				165					170					175	
Trp	Val	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Val	His	Cys	Ser	Val	Lys	Ser
			180					185					190		
Glu	His	Ser	Ala	Ala	Ala	Lys	Thr	Gly	Gly	Cys	Phe	Pro	Ala	Gly	Ala
		195					200					205			
Gln	Val	Arg	Leu	Glu	Asn	Gly	Glu	Arg	Val	Ala	Leu	Ser	Ala	Val	Lys
	210					215					220				
Pro	Gly	Asp	Arg	Val	Leu	Ala	Met	Gly	Glu	Asp	Gly	Thr	Pro	Thr	Phe
225					230					235					240
Ser	Asp	Val	Leu	Ile	Phe	Leu	Asp	Arg	Glu	Pro	Asn	Arg	Leu	Arg	Ala
				245					250					255	
Phe	Gln	Val	Ile	Glu	Thr	Gln	Asp	Pro	Pro	Arg	Arg	Leu	Ala	Leu	Thr
			260					265					270		
Pro	Ala	His	Leu	Leu	Phe	Ile	Ala	Asp	Asn	His	Thr	Glu	Pro	Ala	Ala
		275					280					285			
His	Phe	Arg	Ala	Thr	Phe	Ala	Ser	His	Val	Gln	Pro	Gly	Gln	Tyr	Val
	290					295					300				
Leu	Val	Ser	Gly	Val	Pro	Gly	Leu	Gln	Pro	Ala	Arg	Val	Ala	Ala	Val
305					310					315					320
Ser	Thr	His	Val	Ala	Leu	Gly	Ser	Tyr	Ala	Pro	Leu	Thr	Arg	His	Gly

a069seq
330

325

335

Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala
340 345 350

Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe Pro
355 360 365

Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr
370 375 380

Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Ser Thr
385 390 395 400

Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser
405 410

<210> 13

<211> 437

<212> PRT

<213> Murine sp.

<400> 13

Met Leu Leu Leu Leu Ala Arg Cys Phe Leu Val Ile Leu Ala Ser Ser
1 5 10 15

Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly
20 25 30

Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe
35 40 45

Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu
50 55 60

Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn
65 70 75 80

Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp
85 90 95

Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile
100 105 110

Ser Val Met Asn Gln Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
115 120 125

Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly
130 135 140

Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly

a069seq

145					150					155					160
Met	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr
				165					170					175	
Glu	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val
			180					185					190		
Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val	His	Leu
		195					200					205			
Glu	Gln	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Arg
	210					215					220				
Val	Leu	Ala	Ala	Asp	Asp	Gln	Gly	Arg	Leu	Leu	Tyr	Ser	Asp	Phe	Leu
225					230					235					240
Thr	Phe	Leu	Asp	Arg	Asp	Glu	Gly	Ala	Lys	Lys	Val	Phe	Tyr	Val	Ile
				245					250					255	
Glu	Thr	Leu	Glu	Pro	Arg	Glu	Arg	Leu	Leu	Leu	Thr	Ala	Ala	His	Leu
			260					265					270		
Leu	Phe	Val	Ala	Pro	His	Asn	Asp	Ser	Gly	Pro	Thr	Pro	Gly	Pro	Ser
		275					280					285			
Ala	Leu	Phe	Ala	Ser	Arg	Val	Arg	Pro	Gly	Gln	Arg	Val	Tyr	Val	Val
	290					295					300				
Ala	Glu	Arg	Gly	Gly	Asp	Arg	Arg	Leu	Leu	Pro	Ala	Ala	Val	His	Ser
305					310					315					320
Val	Thr	Leu	Arg	Glu	Glu	Glu	Ala	Gly	Ala	Tyr	Ala	Pro	Leu	Thr	Ala
				325					330					335	
His	Gly	Thr	Ile	Leu	Ile	Asn	Arg	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val
			340					345					350		
Ile	Glu	Glu	His	Ser	Trp	Ala	His	Arg	Ala	Phe	Ala	Pro	Phe	Arg	Leu
		355					360					365			
Ala	His	Ala	Leu	Leu	Ala	Ala	Leu	Ala	Pro	Ala	Arg	Thr	Asp	Gly	Gly
	370					375					380				
Gly	Gly	Gly	Ser	Ile	Pro	Ala	Ala	Gln	Ser	Ala	Thr	Glu	Ala	Arg	Gly
385					390					395					400
Ala	Glu	Pro	Thr	Ala	Gly	Ile	His	Trp	Tyr	Ser	Gln	Leu	Leu	Tyr	His
				405					410					415	
Ile	Gly	Thr	Trp	Leu	Leu	Asp	Ser	Glu	Thr	Met	His	Pro	Leu	Gly	Met

a069seq
425

420

430

Ala Val Lys Ser Ser
435

<210> 14

<211> 418

<212> PRT

<213> zebrafish sp.

<400> 14

Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser
1 5 10 15

Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg
20 25 30

Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
35 40 45

Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
50 55 60

Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
65 70 75 80

Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
85 90 95

Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser
100 105 110

Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp
115 120 125

Asp Glu Asp Gly His His Phe Glu Glu Ser Leu His Tyr Glu Gly Arg
130 135 140

Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys Tyr Gly Thr
145 150 155 160

Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu
165 170 175

Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala
180 185 190

Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Leu Val Ser Leu Gln
195 200 205

Asp Gly Gly Gln Lys Ala Val Lys Asp Leu Asn Pro Gly Asp Lys Val

a069seq

210		215		220
Leu Ala Ala Asp Ser Ala Gly Asn Leu Val Phe Ser Asp Phe Ile Met				
225		230		240
Phe Thr Asp Arg Asp Ser Thr Thr Arg Arg Val Phe Tyr Val Ile Glu				
	245		250	255
Thr Gln Glu Pro Val Glu Lys Ile Thr Leu Thr Ala Ala His Leu Leu				
	260		265	270
Phe Val Leu Asp Asn Ser Thr Glu Asp Leu His Thr Met Thr Ala Ala				
	275		280	285
Tyr Ala Ser Ser Val Arg Ala Gly Gln Lys Val Met Val Val Asp Asp				
	290		295	300
Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr Glu Glu				
305		310		320
Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile Val Val				
	325		330	335
Asp Arg Ile Leu Ala Ser Cys Tyr Ala Val Ile Glu Asp Gln Gly Leu				
	340		345	350
Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Tyr Val Ser Ser				
	355		360	365
Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn				
	370		375	380
Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr				
385		390		400
Trp Leu Leu Asp Ser Asn Met Leu His Pro Leu Gly Met Ser Val Asn				
	405		410	415

Ser Ser

<210> 15

<211> 475

<212> PRT

<213> Homo sapiens

<220>

<223> Xaa at position 463 is any or unknown amino acid

<400> 15

Met	Leu	Leu	Leu	Ala	Arg	Cys	Leu	Leu	Leu	Val	Leu	Val	Ser	Ser	Leu
1				5						10					15

a069seq

Leu	Val	Cys	Ser	Gly	Leu	Ala	Cys	Gly	Pro	Gly	Arg	Gly	Phe	Gly	Lys		
		20						25					30				
Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe	Ile		
		35					40					45					
Pro	Asn	Val	Ala	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	Tyr	Glu	Gly		
	50					55					60						
Lys	Ile	Ser	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	Tyr		
65					70					75					80		
Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	Arg		
				85					90					95			
Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ala	Leu	Ala	Ile	Ser		
			100					105					110				
Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	Glu	Gly	Trp		
		115					120					125					
Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg		
	130					135					140						
Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Ser	Lys	Tyr	Gly	Met		
145					150					155					160		
Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu		
			165						170					175			
Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	Ala		
			180					185					190				
Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val	His	Leu	Glu		
		195					200					205					
Gln	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Ser	Pro	Gly	Asp	Arg	Val		
	210					215					220						
Leu	Ala	Ala	Asp	Asp	Gln	Gly	Arg	Leu	Leu	Tyr	Ser	Asp	Phe	Leu	Thr		
225					230					235					240		
Phe	Leu	Asp	Arg	Asp	Asp	Gly	Ala	Lys	Lys	Val	Phe	Tyr	Val	Ile	Glu		
				245					250					255			
Thr	Arg	Glu	Pro	Arg	Glu	Arg	Leu	Leu	Leu	Thr	Ala	Ala	His	Leu	Leu		
			260					265					270				
Phe	Val	Ala	Pro	His	Asn	Asp	Ser	Ala	Thr	Gly	Glu	Pro	Glu	Ala	Ser		
		275					280					285					

a069seq

Ser Gly Ser Gly Pro Pro Ser Gly Gly Ala Leu Gly Pro Arg Ala Leu
 290 295 300
 Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val Ala Glu
 305 310 315 320
 Arg Asp Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser Val Thr
 325 330 335
 Leu Ser Glu Glu Ala Ala Gly Ala Tyr Ala Pro Leu Thr Ala Gln Gly
 340 345 350
 Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val Ile Glu
 355 360 365
 Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu Ala His
 370 375 380
 Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Arg Gly Gly Asp
 385 390 395 400
 Ser Gly Gly Gly Asp Arg Gly Gly Gly Gly Gly Arg Val Ala Leu Thr
 405 410 415
 Ala Pro Gly Ala Ala Asp Ala Pro Gly Ala Gly Ala Thr Ala Gly Ile
 420 425 430
 His Trp Tyr Ser Gln Leu Leu Tyr Gln Ile Gly Thr Trp Leu Leu Asp
 435 440 445
 Ser Glu Ala Leu His Pro Leu Gly Met Ala Val Lys Ser Ser Xaa Ser
 450 455 460
 Arg Gly Ala Gly Gly Gly Ala Arg Glu Gly Ala
 465 470 475

<210> 16

<211> 411

<212> PRT

<213> Homo sapiens

<400> 16

Met Ser Pro Ala Arg Leu Arg Pro Arg Leu His Phe Cys Leu Val Leu
 1 5 10 15
 Leu Leu Leu Leu Val Val Pro Ala Ala Trp Gly Cys Gly Pro Gly Arg
 20 25 30
 Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
 35 40 45

a069seq

Tyr	Lys	Gln	Phe	Ser	Pro	Asn	Val	Pro	Glu	Lys	Thr	Leu	Gly	Ala	Ser		
	50					55					60						
Gly	Arg	Tyr	Glu	Gly	Lys	Ile	Ala	Arg	Ser	Ser	Glu	Arg	Phe	Lys	Glu		
65					70					75					80		
Leu	Thr	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn		
				85					90					95			
Thr	Gly	Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Arg	Leu	Asn		
			100					105					110				
Ser	Leu	Ala	Ile	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg		
		115					120					125					
Val	Thr	Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu		
	130					135					140						
His	Tyr	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg		
145					150					155					160		
Asn	Lys	Tyr	Gly	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp		
				165					170					175			
Trp	Val	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Val	His	Cys	Ser	Val	Lys	Ser		
			180					185					190				
Glu	His	Ser	Ala	Ala	Ala	Lys	Thr	Gly	Gly	Cys	Phe	Pro	Ala	Gly	Ala		
		195					200					205					
Gln	Val	Arg	Leu	Glu	Ser	Gly	Ala	Arg	Val	Ala	Leu	Ser	Ala	Val	Arg		
	210					215					220						
Pro	Gly	Asp	Arg	Val	Leu	Ala	Met	Gly	Glu	Asp	Gly	Ser	Pro	Thr	Phe		
225					230					235					240		
Ser	Asp	Val	Leu	Ile	Phe	Leu	Asp	Arg	Glu	Pro	His	Arg	Leu	Arg	Ala		
				245					250					255			
Phe	Gln	Val	Ile	Glu	Thr	Gln	Asp	Pro	Pro	Arg	Arg	Leu	Ala	Leu	Thr		
			260					265					270				
Pro	Ala	His	Leu	Leu	Phe	Thr	Ala	Asp	Asn	His	Thr	Glu	Pro	Ala	Ala		
		275					280					285					
Arg	Phe	Arg	Ala	Thr	Phe	Ala	Ser	His	Val	Gln	Pro	Gly	Gln	Tyr	Val		
	290					295					300						
Leu	Val	Ala	Gly	Val	Pro	Gly	Leu	Gln	Pro	Ala	Arg	Val	Ala	Ala	Val		
305					310					315					320		

a069seq

Ser Thr His Val Ala Leu Gly Ala Tyr Ala Pro Leu Thr Lys His Gly
325 330 335

Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala
340 345 350

Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe His
355 360 365

Ser Leu Ala Trp Gly Ser Trp Thr Pro Gly Glu Gly Val His Trp Tyr
370 375 380

Pro Gln Leu Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Gly Ser
385 390 395 400

Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser
405 410

<210> 17

<211> 396

<212> PRT

<213> Homo sapiens

<400> 17

Met Ala Leu Leu Thr Asn Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
1 5 10 15

Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
20 25 30

Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
35 40 45

Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
50 55 60

Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
65 70 75 80

Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
85 90 95

Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
100 105 110

Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
115 120 125

Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
130 135 140

a069seq

Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly
145					150					155					160
Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr
				165					170					175	
Glu	Ser	Arg	Asn	His	Val	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu
			180					185					190		
Ala	Val	Arg	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu
		195					200					205			
Trp	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp
	210					215					220				
Val	Leu	Ala	Ala	Asp	Ala	Ser	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu
225					230					235					240
Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val
				245					250					255	
Glu	Thr	Glu	Trp	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu
			260					265					270		
Val	Phe	Ala	Ala	Arg	Gly	Pro	Ala	Pro	Ala	Pro	Gly	Asp	Phe	Ala	Pro
		275					280					285			
Val	Phe	Ala	Arg	Arg	Leu	Arg	Ala	Gly	Asp	Ser	Val	Leu	Ala	Pro	Gly
	290					295					300				
Gly	Asp	Ala	Leu	Arg	Pro	Ala	Arg	Val	Ala	Arg	Val	Ala	Arg	Glu	Glu
305					310					315					320
Ala	Val	Gly	Val	Phe	Ala	Pro	Leu	Thr	Ala	His	Gly	Thr	Leu	Leu	Val
				325					330					335	
Asn	Asp	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Leu	Glu	Ser	His	Gln	Trp
			340					345					350		
Ala	His	Arg	Ala	Phe	Ala	Pro	Leu	Arg	Leu	Leu	His	Ala	Leu	Gly	Ala
		355					360					365			
Leu	Leu	Pro	Gly	Gly	Ala	Val	Gln	Pro	Thr	Gly	Met	His	Trp	Tyr	Ser
	370					375					380				
Arg	Leu	Leu	Tyr	Arg	Leu	Ala	Glu	Glu	Leu	Leu	Gly				
385					390						395				

<210> 18

<211> 416

a069seq

<212> PRT

<213> Zebrafish sp.

<400> 18

Met	Asp	Val	Arg	Leu	His	Leu	Lys	Gln	Phe	Ala	Leu	Leu	Cys	Phe	Ile	1	5	10	15
Ser	Leu	Leu	Leu	Thr	Pro	Cys	Gly	Leu	Ala	Cys	Gly	Pro	Gly	Arg	Gly	20	25	30	
Tyr	Gly	Lys	Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	35	40	45	
Gln	Phe	Ile	Pro	Asn	Val	Ala	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Lys	50	55	60	
Tyr	Glu	Gly	Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Ile	65	70	75	80
Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Asn	85	90	95	
Ala	Asp	Arg	Leu	Met	Thr	Lys	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ser	Leu	100	105	110	
Ala	Ile	Ser	Val	Met	Asn	His	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	115	120	125	
Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	Leu	Glu	Glu	Ser	Leu	His	Tyr	130	135	140	
Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Lys	Ser	Lys	145	150	155	160
Tyr	Gly	Met	Leu	Ser	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	165	170	175	
Tyr	Tyr	Glu	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	180	185	190	
Ser	Val	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Gly	Thr	Val	195	200	205	
Thr	Leu	Gly	Asp	Gly	Thr	Arg	Lys	Pro	Ile	Lys	Asp	Leu	Lys	Val	Gly	210	215	220	
Asp	Arg	Val	Leu	Ala	Ala	Asp	Glu	Lys	Gly	Asn	Val	Leu	Ile	Ser	Asp	225	230	235	240
Phe	Ile	Met	Phe	Ile	Asp	His	Asp	Pro	Thr	Thr	Arg	Arg	Gln	Phe	Ile	245	250	255	

a069seq

Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala
260 265 270

His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala
275 280 285

Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu
290 295 300

Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr
305 310 315 320

Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile
325 330 335

Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His
340 345 350

Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu
355 360 365

Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu
370 375 380

Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp
385 390 395 400

Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser
405 410 415

<210> 19
<211> 1416
<212> DNA
<213> Drosophila sp.

<220>
<221> CDS
<222> (1)..(1413)

<400> 19
atg gat aac cac agc tca gtg cct tgg gcc agt gcc gcc agt gtc acc 48

Met Asp Asn His Ser Ser Val Pro Trp Ala Ser Ala Ala Ser Val Thr
1 5 10 15

tgt ctc tcc ctg gga tgc caa atg cca cag ttc cag ttc cag ttc cag 96

Cys Leu Ser Leu Gly Cys Gln Met Pro Gln Phe Gln Phe Gln Phe Gln
20 25 30

a069seq

ctc	caa	atc	cgc	agc	gag	ctc	cat	ctc	cgc	aag	ccc	gca	aga	aga	acg	144
Leu	Gln	Ile	Arg	Ser	Glu	Leu	His	Leu	Arg	Lys	Pro	Ala	Arg	Arg	Thr	
	35						40					45				
caa	acg	atg	cgc	cac	att	gcg	cat	acg	cag	cgt	tgc	ctc	agc	agg	ctg	192
Gln	Thr	Met	Arg	His	Ile	Ala	His	Thr	Gln	Arg	Cys	Leu	Ser	Arg	Leu	
	50					55					60					
acc	tct	ctg	gtg	gcc	ctg	ctg	ctg	atc	gtc	ttg	ccg	atg	gtc	ttt	agc	240
Thr	Ser	Leu	Val	Ala	Leu	Leu	Leu	Ile	Val	Leu	Pro	Met	Val	Phe	Ser	
65					70					75					80	
ccg	gct	cac	agc	tgc	ggc	cct	ggc	cga	gga	ttg	ggc	cgt	cat	agg	gcg	288
Pro	Ala	His	Ser	Cys	Gly	Pro	Gly	Arg	Gly	Leu	Gly	Arg	His	Arg	Ala	
				85					90					95		
cgc	aac	ctg	tat	ccg	ctg	gtc	ctc	aag	cag	aca	att	ccc	aat	cta	tcc	336
Arg	Asn	Leu	Tyr	Pro	Leu	Val	Leu	Lys	Gln	Thr	Ile	Pro	Asn	Leu	Ser	
			100					105					110			
gag	tac	acg	aac	agc	gcc	tcc	gga	cct	ctg	gag	ggc	gtg	atc	cgt	cgg	384
Glu	Tyr	Thr	Asn	Ser	Ala	Ser	Gly	Pro	Leu	Glu	Gly	Val	Ile	Arg	Arg	
		115					120					125				
gat	tcg	ccc	aaa	ttc	aag	gac	ctc	gtg	ccc	aac	tac	aac	agg	gac	atc	432
Asp	Ser	Pro	Lys	Phe	Lys	Asp	Leu	Val	Pro	Asn	Tyr	Asn	Arg	Asp	Ile	
	130					135					140					
ctt	ttc	cgt	gac	gag	gaa	ggc	acc	gga	gcg	gat	ggc	ttg	atg	agc	aag	480
Leu	Phe	Arg	Asp	Glu	Glu	Gly	Thr	Gly	Ala	Asp	Gly	Leu	Met	Ser	Lys	
145					150					155					160	
cgc	tgc	aag	gag	aag	cta	aac	gtg	ctg	gcc	tac	tcg	gtg	atg	aac	gaa	528
Arg	Cys	Lys	Glu	Lys	Leu	Asn	Val	Leu	Ala	Tyr	Ser	Val	Met	Asn	Glu	
				165					170					175		
tgg	ccc	ggc	atc	cgg	ctg	ctg	gtc	acc	gag	agc	tgg	gac	gag	gac	tac	576
Trp	Pro	Gly	Ile	Arg	Leu	Leu	Val	Thr	Glu	Ser	Trp	Asp	Glu	Asp	Tyr	
			180					185					190			

a069seq

cat cac ggc cag gag tcg ctc cac tac gag ggc cga gcg gtg acc att	624
His His Gly Gln Glu Ser Leu His Tyr Glu Gly Arg Ala Val Thr Ile 195 200 205	
gcc acc tcc gat cgc gac cag tcc aaa tac ggc atg ctc gct cgc ctg	672
Ala Thr Ser Asp Arg Asp Gln Ser Lys Tyr Gly Met Leu Ala Arg Leu 210 215 220	
gcc gtc gag gct gga ttc gat tgg gtc tcc tac gtc agc agg cgc cac	720
Ala Val Glu Ala Gly Phe Asp Trp Val Ser Tyr Val Ser Arg Arg His 225 230 235 240	
atc tac tgc tcc gtc aag tca gat tcg tcg atc agt tcc cac gtg cac	768
Ile Tyr Cys Ser Val Lys Ser Asp Ser Ser Ile Ser Ser His Val His 245 250 255	
ggc tgc ttc acg ccg gag agc aca gcg ctg ctg gag agt gga gtc cgg	816
Gly Cys Phe Thr Pro Glu Ser Thr Ala Leu Leu Glu Ser Gly Val Arg 260 265 270	
aag ccg ctc ggc gag ctc tct atc gga gat cgt gtt ttg agc atg acc	864
Lys Pro Leu Gly Glu Leu Ser Ile Gly Asp Arg Val Leu Ser Met Thr 275 280 285	
gcc aac gga cag gcc gtc tac agc gaa gtg atc ctc ttc atg gac cgc	912
Ala Asn Gly Gln Ala Val Tyr Ser Glu Val Ile Leu Phe Met Asp Arg 290 295 300	
aac ctc gag cag atg caa aac ttt gtg cag ctg cac acg gac ggt gga	960
Asn Leu Glu Gln Met Gln Asn Phe Val Gln Leu His Thr Asp Gly Gly 305 310 315 320	
gca gtg ctc acg gtg acg ccg gct cac ctg gtt agc gtt tgg cag ccg	1008
Ala Val Leu Thr Val Thr Pro Ala His Leu Val Ser Val Trp Gln Pro 325 330 335	
gag agc cag aag ctc acg ttt gtg ttt gcg cat cgc atc gag gag aag	1056
Glu Ser Gln Lys Leu Thr Phe Val Phe Ala His Arg Ile Glu Glu Lys 340 345 350	
aac cag gtg ctc gta cgg gat gtg gag acg ggc gag ctg agg ccc cag	1104

a069seq

Asn	Gln	Val	Leu	Val	Arg	Asp	Val	Glu	Thr	Gly	Glu	Leu	Arg	Pro	Gln		
		355					360					365					
cga	gtg	gtc	aag	ttg	ggc	agt	gtg	cgc	agt	aag	ggc	gtg	gtc	gcg	ccg	1152	
Arg	Val	Val	Lys	Leu	Gly	Ser	Val	Arg	Ser	Lys	Gly	Val	Val	Ala	Pro		
	370					375					380						
ctg	acc	cgc	gag	ggc	acc	att	gtg	gtc	aac	tcg	gtg	gcc	gcc	agt	tgc	1200	
Leu	Thr	Arg	Glu	Gly	Thr	Ile	Val	Val	Asn	Ser	Val	Ala	Ala	Ser	Cys		
385					390					395					400		
tat	gcg	gtg	atc	aac	agt	cag	tcg	ctg	gcc	cac	tgg	gga	ctg	gct	ccc	1248	
Tyr	Ala	Val	Ile	Asn	Ser	Gln	Ser	Leu	Ala	His	Trp	Gly	Leu	Ala	Pro		
				405					410					415			
atg	cgc	ctg	ctg	tcc	acg	ctg	gag	gcg	tgg	ctg	ccc	gcc	aag	gag	cag	1296	
Met	Arg	Leu	Leu	Ser	Thr	Leu	Glu	Ala	Trp	Leu	Pro	Ala	Lys	Glu	Gln		
			420					425					430				
ttg	cac	agt	tcg	ccg	aag	gtg	gtg	agc	tcg	gcg	cag	cag	cag	aat	ggc	1344	
Leu	His	Ser	Ser	Pro	Lys	Val	Val	Ser	Ser	Ala	Gln	Gln	Gln	Asn	Gly		
		435					440					445					
atc	cat	tgg	tat	gcc	aat	gcg	ctc	tac	aag	gtc	aag	gac	tac	gtg	ctg	1392	
Ile	His	Trp	Tyr	Ala	Asn	Ala	Leu	Tyr	Lys	Val	Lys	Asp	Tyr	Val	Leu		
	450					455					460						
ccg	cag	agc	tgg	cgc	cac	gat	tga									1416	
Pro	Gln	Ser	Trp	Arg	His	Asp											
465					470												

<210> 20
 <211> 471
 <212> PRT
 <213> Drosophila sp.

<400> 20
 Met Asp Asn His Ser Ser Val Pro Trp Ala Ser Ala Ala Ser Val Thr
 1 5 10 15
 Cys Leu Ser Leu Gly Cys Gln Met Pro Gln Phe Gln Phe Gln Phe Gln
 20 25 30

a069seq

Asn	Leu	Glu	Gln	Met	Gln	Asn	Phe	Val	Gln	Leu	His	Thr	Asp	Gly	Gly	305	310	315	320
Ala	Val	Leu	Thr	Val	Thr	Pro	Ala	His	Leu	Val	Ser	Val	Trp	Gln	Pro	325	330	335	
Glu	Ser	Gln	Lys	Leu	Thr	Phe	Val	Phe	Ala	His	Arg	Ile	Glu	Glu	Lys	340	345	350	
Asn	Gln	Val	Leu	Val	Arg	Asp	Val	Glu	Thr	Gly	Glu	Leu	Arg	Pro	Gln	355	360	365	
Arg	Val	Val	Lys	Leu	Gly	Ser	Val	Arg	Ser	Lys	Gly	Val	Val	Ala	Pro	370	375	380	
Leu	Thr	Arg	Glu	Gly	Thr	Ile	Val	Val	Asn	Ser	Val	Ala	Ala	Ser	Cys	385	390	395	400
Tyr	Ala	Val	Ile	Asn	Ser	Gln	Ser	Leu	Ala	His	Trp	Gly	Leu	Ala	Pro	405	410	415	
Met	Arg	Leu	Leu	Ser	Thr	Leu	Glu	Ala	Trp	Leu	Pro	Ala	Lys	Glu	Gln	420	425	430	
Leu	His	Ser	Ser	Pro	Lys	Val	Val	Ser	Ser	Ala	Gln	Gln	Gln	Asn	Gly	435	440	445	
Ile	His	Trp	Tyr	Ala	Asn	Ala	Leu	Tyr	Lys	Val	Lys	Asp	Tyr	Val	Leu	450	455	460	
Pro	Gln	Ser	Trp	Arg	His	Asp										465	470		

<210> 21

<211> 221

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: degenerate polypeptide sequence

<220>

<222> 7

<223> Gly, Ala, Val, Leu, Ile, Phe, Tyr or Trp

<220>

<222> 9

<223> Arg, His or Lys

a069seq

<220>
<222> 44
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<222> 85
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<222> 93
<223> Lys, Arg, His, Asn or Gln

<220>
<222> 98
<223> Lys, Arg or His

<220>
<222> 112
<223> Ser, Thr, Tyr, Trp or Phe

<220>
<222> 132
<223> Lys, Arg or His

<220>
<222> 137
<223> Met, Cys, Ser or Thr

<220>
<222> 139
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<222> 181
<223> Leu, Val, Met, Thr or Ser

<220>
<222> 183
<223> His, Phe, Tyr, Ser, Thr, Met or Cys

<220>
<222> 185
<223> Gln, Asn, Glu, or Asp

<220>
<222> 186
<223> His, Phe, Tyr, Thr, Gln, Asn, Glu or Asp

<220>
<222> 189

a069seq

<223> Gln, Asn, Glu, Asp, Thr, Ser, Met or Cys

<220>

<222> 191

<223> Ala, Gly, Cys, Leu, Val or Met

<220>

<222> 196

<223> Arg, Lys, Met, Ile, Asn, Asp, Glu, Gln, Ser, Thr or Cys

<220>

<222> 200

<223> Arg, Lys, Met or Ile

<220>

<222> 206

<223> Ala, Gly, Cys, Asp, Glu, Gln, Asn, Ser, Thr or Met

<220>

<222> 207

<223> Ala, Gly, Cys, Asp, Asn, Glu or Gln

<220>

<222> 209

<223> Arg, Lys, Met, Ile, Asn, Asp, Glu or Gln

<220>

<222> 211

<223> Leu, Val, Met or Ile

<220>

<222> 212

<223> Phe, Tyr, Thr, His or Trp

<220>

<222> 216

<223> Ile, Val, Leu or Met

<220>

<222> 217

<223> Met, Cys, Ile, Leu, Val, Thr or Ser

<220>

<222> 219

<223> Leu, Val, Met, Thr or Ser

<220>

<223> each Xaa may also be any amino acid.

<400> 21

Cys Gly Pro Gly Arg Gly Xaa Gly Xaa Arg Arg His Pro Lys Lys Leu

a069seq

1		5		10		15									
Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe	Ile	Pro	Asn	Val	Ala	Glu	Lys	Thr
		20						25					30		
Leu	Gly	Ala	Ser	Gly	Arg	Tyr	Glu	Gly	Lys	Ile	Xaa	Arg	Asn	Ser	Glu
		35					40					45			
Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys
	50					55					60				
Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys
65					70					75					80
Asp	Lys	Leu	Asn	Xaa	Leu	Ala	Ile	Ser	Val	Met	Asn	Xaa	Trp	Pro	Gly
				85					90					95	
Val	Xaa	Leu	Arg	Val	Thr	Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	Xaa
			100					105					110		
Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser
		115					120					125			
Asp	Arg	Asp	Xaa	Ser	Lys	Tyr	Gly	Xaa	Leu	Xaa	Arg	Leu	Ala	Val	Glu
	130					135					140				
Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Ile	His	Cys
145					150					155					160
Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe
			165						170					175	
Pro	Gly	Ser	Ala	Xaa	Val	Xaa	Leu	Xaa	Xaa	Gly	Gly	Xaa	Lys	Xaa	Val
			180					185					190		
Lys	Asp	Leu	Xaa	Pro	Gly	Asp	Xaa	Val	Leu	Ala	Ala	Asp	Xaa	Xaa	Gly
		195					200					205			
Xaa	Leu	Xaa	Xaa	Ser	Asp	Phe	Xaa	Xaa	Phe	Xaa	Asp	Arg			
	210					215					220				

<210> 22

<211> 167

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: degenerate polypeptide sequence

a069seq

<220>

<222> 7

<223> Gly, Ala, Val, Leu, Ile, Pro, Phe or Tyr

<220>

<222> 8

<223> Gly, Ala, Val, Leu or Ile

<220>

<222> 9

<223> Gly, Ala, Val, Leu, Ile, Lys, His or Arg

<220>

<222> 12

<223> Lys, Arg or His

<220>

<222> 13

<223> Phe, Trp, Tyr or an amino acid gap

<220>

<222> 14

<223> Gly, Ala, Val, Leu, Ile or an amino acid gap

<220>

<222> 17

<223> Asn, Gln, His, Arg or Lys

<220>

<222> 19

<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>

<222> 22

<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>

<222> 27

<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>

<222> 29

<223> Ser, Thr, Gln or Asn

<220>

<222> 30

<223> Met, Cys, Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>

<222> 31

<223> Gly, Ala, Val, Leu, Ile or Pro

a069seq

<220>

<222> 33

<223> Arg, His or Lys

<220>

<222> 40

<223> Gly, Ala, Val, Leu, Ile, Pro, Arg, His or Lys

<220>

<222> 41

<223> Gly, Ala, Val, Leu, Ile, Phe or Tyr

<220>

<222> 44

<223> Arg, His or Lys

<220>

<222> 45

<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>

<222> 46

<223> Thr or Ser

<220>

<222> 48

<223> Gly, Ala, Val, Leu, Ile, Asn or Gln

<220>

<222> 53

<223> Arg, His or Lys

<220>

<222> 54

<223> Asp or Glu

<220>

<222> 71

<223> Ser or Thr

<220>

<222> 79

<223> Glu, Asp, Gln or Asn

<220>

<222> 83

<223> Glu or Asp

<220>

<222> 84

a069seq

<223> Arg, His or Lys

<220>

<222> 85

<223> Gly, Ala, Val, Leu or Ile

<220>

<222> 87

<223> Gly, Ala, Val, Leu, Ile, Thr or Ser

<220>

<222> 95

<223> Met, Cys, Gln, Asn, Arg, Lys or His

<220>

<222> 100

<223> Arg, His or Lys

<220>

<222> 107

<223> Trp, Phe, Tyr, Arg, His or Lys

<220>

<222> 114

<223> Gly, Ala, Val, Leu, Ile, Ser, Thr, Tyr or Phe

<220>

<222> 115

<223> Gln, Asn, Asp or Glu

<220>

<222> 116

<223> Asp or Glu

<220>

<222> 125

<223> Gly, Ala, Val, Leu, or Ile

<220>

<222> 134

<223> Arg, His or Lys

<220>

<222> 135

<223> Asn, Gln, Thr or Ser

<220>

<222> 139

<223> Gly, Ala, Val, Leu, Ile, Ser, Thr, Met or Cys

<220>

a069seq

<222> 141
 <223> Gly, Ala, Val, Leu, Ile, Thr or Ser

<220>
 <222> 157
 <223> Arg, His or Lys

<220>
 <222> 158
 <223> Asn, Gln, Gly, Ala, Val, Leu or Ile

<220>
 <222> 160
 <223> Gly, Ala, Val, Leu or Ile

<220>
 <222> 162
 <223> Gly, Ala, Val, Leu, Ile, Ser, Thr or Cys

<220>
 <222> 166
 <223> Gly, Ala, Val, Leu, Ile, Thr or Ser

<220>
 <222> 167
 <223> Asp or Glu

<400> 22
 Cys Gly Pro Gly Arg Gly Xaa Xaa Xaa Arg Arg Xaa Xaa Xaa Pro Lys
 1 5 10 15
 Xaa Leu Xaa Pro Leu Xaa Tyr Lys Gln Phe Xaa Pro Xaa Xaa Xaa Glu
 20 25 30
 Xaa Thr Leu Gly Ala Ser Gly Xaa Xaa Glu Gly Xaa Xaa Xaa Arg Xaa
 35 40 45
 Ser Glu Arg Phe Xaa Xaa Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile
 50 55 60
 Phe Lys Asp Glu Glu Asn Xaa Gly Ala Asp Arg Leu Met Thr Xaa Arg
 65 70 75 80
 Cys Lys Xaa Xaa Xaa Asn Xaa Leu Ala Ile Ser Val Met Asn Xaa Trp
 85 90 95
 Pro Gly Val Xaa Leu Arg Val Thr Glu Gly Xaa Asp Glu Asp Gly His
 100 105 110
 His Xaa Xaa Xaa Ser Leu His Tyr Glu Gly Arg Ala Xaa Asp Ile Thr
 115 120 125

a069seq

Thr	Ser	Asp	Arg	Asp	Xaa	Xaa	Lys	Tyr	Gly	Xaa	Leu	Xaa	Arg	Leu	Ala
130						135					140				
Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu	Ser	Xaa	Xaa	His	Xaa
145					150					155					160
His	Xaa	Ser	Val	Lys	Xaa	Xaa									
				165											